## **CLAIMS**

## What is claimed is:

suba.

A method for identifying relative binding motifs of peptide-like molecules, comprising the steps of:

- (a) training an artificial neural network (ANN) with a set of training peptide-like molecules, each of known sequence and binding affinity;
- (b) applying to the ANN at least one peptide-like molecule, each of known sequence but unknown binding affinity;
- (c) analyzing each applied test peptide-like molecule using the ANN to predict a relative binding affinity for each test peptide-like molecule.
- 2. A method for identifying relative peptide binding motifs, comprising the steps of:
  - (a) training an artificial neural network (ANN) with a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
  - (b) applying to the ANN at least one peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
  - (c) analyzing each applied test peptide using the ANN to predict a relative binding affinity for each test peptide.

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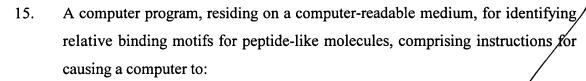
- 3. The method of claim 2, wherein the set of training peptides include peptides having a binding affinity for MHC class I molecules.
- 4. The method of claim 3, wherein the peptides included in the set of training peptides have a binding affinity for mouse MHC class IK<sup>b</sup>.
- 5. The method of claim 2, wherein the set of test peptides include peptides having a binding affinity for MHC class molecules.
- 6. The method of claim 5, wherein the peptides included in the set of test peptides have a binding affinity for mouse MHC class I K<sup>b</sup>.
- 7. The method of claims 1 or 2, wherein the ANN comprises a multi-layer perceptron ANN trained by back-propagation of error.

- 8. A system for identifying relative binding motifs for peptide-like molecules comprising:
  - (a) means for training an artificial neural network (ANN) with a set of training peptide-like molecules, each of known sequence and binding affinity;
  - (b) means for applying to the ANN at least one test peptide-like molecule, each of known sequence but unknown binding affinity;
  - (c) means for analyzing each applied test peptide-like molecule using the ANN to predict a relative binding affinity for each test peptide-like molecule.
- 9. A system for identifying relative peptide binding motifs, comprising:
  - (a) means for training an artificial neural network (ANN) with a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
  - (b) means for applying to the ANN at least one test peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
  - (c) means for analyzing each applied test peptide using the ANN to predict a relative binding affinity for each test peptide.

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- 10. The system of claim 9, wherein the set of training peptides include peptides having a binding affinity for MHC class I molecules.
- 11. The system of claim 10, wherein the peptides included in the set of training peptides have a binding affinity for mouse MHC class I Kb.
- The system of claim 9, wherein the set of test peptides include peptides having a 12. binding affinity for MHC class I molecules.
- The system of claim 12, wherein the peptides included in the set of test peptides 13. have a binding affinity for mouse MHC class I Kb.
- 14. The system of claims 8 or 9, wherein the ANN comprises a multi-layer perceptron ANN trained by back-propagation of error.



- (a) train an artificial neural network (ANN) with a set of training pertide-like molecules, each of known sequence and binding affinity;
- (b) apply to the ANN at least one test peptide-like molecule, each of known sequence but unknown binding affinity;
- (c) analyze each applied test peptide-like molecule using the ANN to predict a relative binding affinity for each test peptide-like molecule.
- 16. A computer program, residing on a computer-readable medium, for identifying relative peptide binding motifs, comprising instructions for causing a computer to:
  - (a) train an artificial neural network (ANN) with a set of training peptides, each of known binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
  - (b) apply to the ANN at least one test peptide, each of unknown binding affinity, each peptide comprising a sequence of amino acids, each amino acid being binary coded as having or lacking specific features generally characteristic of amino acids;
  - (c) analyze each applied test peptide using the ANN to predict a relative binding affinity for each test peptide.

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- 17. The computer program of claim 16, wherein the set of training peptides having a binding affinity for MHC class I molecules.
- 18. The computer program of claim 17, wherein the peptides included in the set of training peptides have a binding affinity for mouse MHC class I K<sup>b</sup>.
- 19. The computer program of claim 16, wherein the set of test peptides include peptides having a binding affinity for MHC class I molecules.
- 20. The computer program of claim 19, wherein the peptides included in the set of test peptides have a binding affinity for mouse MHC class I K<sup>b</sup>.
- 21. The computer program of claims 15 or 16, wherein the ANN comprises a multilayer perceptron ANN trained by back-propagation of error.